

Illustration of an international genetic evaluation robust to inconsistencies of genetic trends in national evaluations

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INTRODUCTION

- ❑ In 2012, S-D MACE model instead of S-MGS model
- ❑ S-D model: - takes better into account dams selection
 - creates new links between countries
- ❑ For most of the countries and most of the traits: changes were small.

For some traits and some bulls: large changes

Some deviations needed to be better understood





AIM OF STUDY

- ❑ Analyze the consistency of MACE EBVs calculated with the S-D model compared to S-MGS model.
- ❑ Make proposals for improving MACE methodology in order to get more robust international comparisons.



I. Impact of the change in model on robustness against biases on genetic trend



DATA

- ❑ Data on Holstein breed from INTERBULL routine evaluation of:
 - December 2011: The last S-MGS MACE
 - April 2012 : The first S-D MACE

- ❑ 4 countries, two traits (protein and longevity)



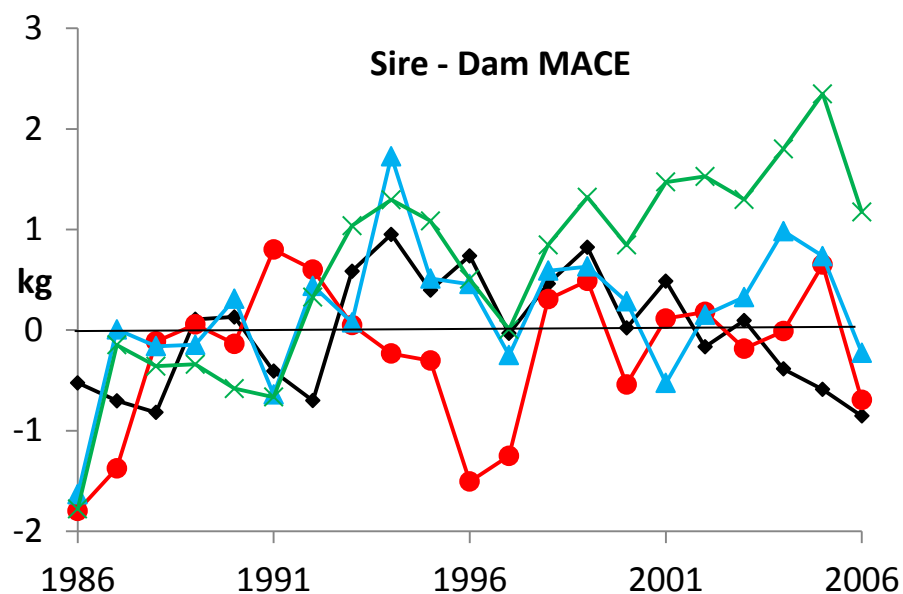
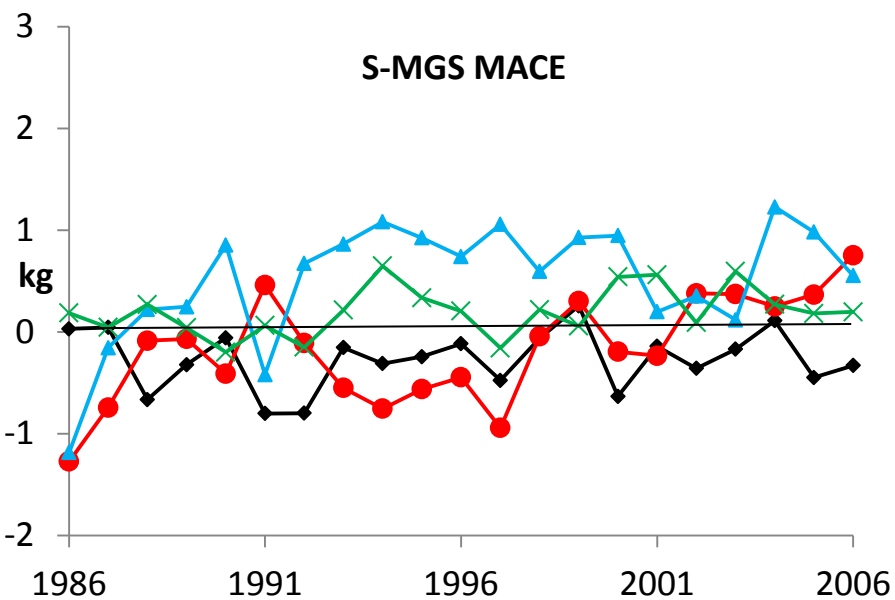
METHODS

- Mendelian Sampling analysis
- Full sibs analysis
- Truncated evaluation

Interbull ran a special evaluation with data from April 2012 official run and cut off year 1995 instead of 1986(longevity)

Mendelian Samplings estimates

PROTEIN



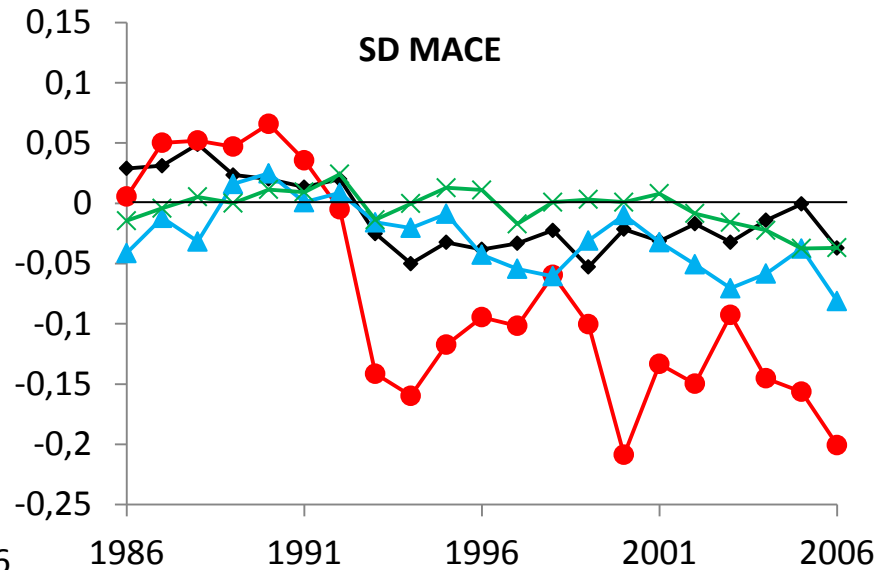
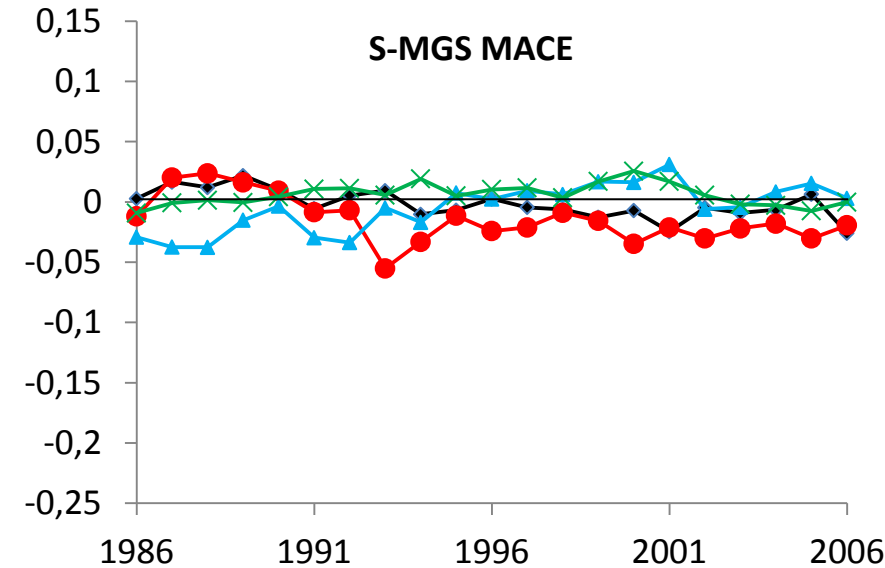
—◆— Country A —●— Country B
—▲— Country C —×— Country D



Mendelian Samplings estimates

LONGEVITY

Gen
std



—●— Country A —●— Country B
—▲— Country C —×— Country D

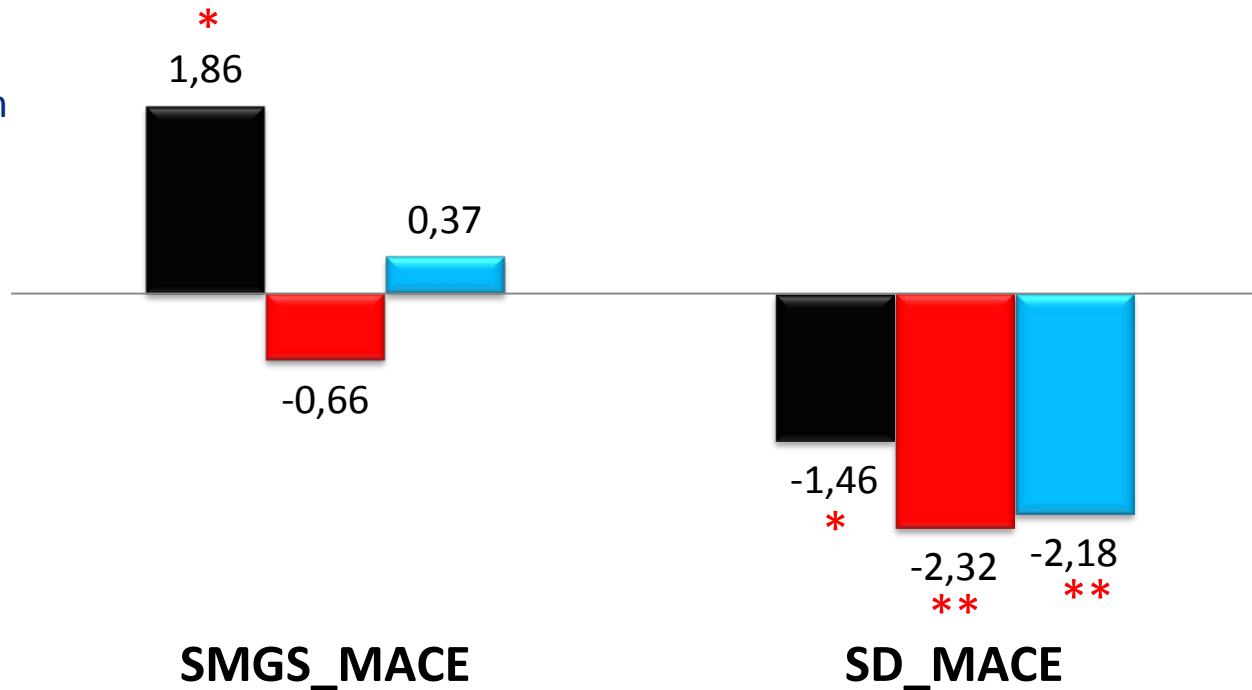


FULL SIBS

PROTEIN YIELD

■ Country_A ■ Country_B ■ country_C

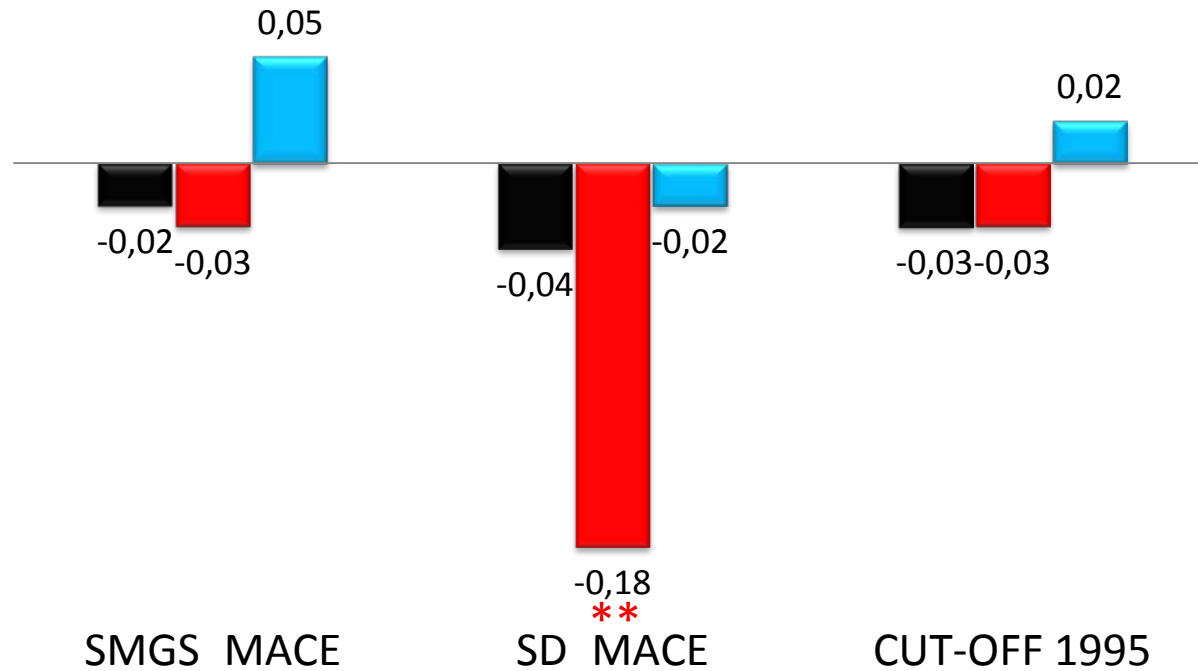
-All bulls with Birth Year >1995
-Deviations from country_D



FULL SIBS

Longevity

■ Country_A
 ■ Country_B
 ■ country_C



-All bulls with Birth Year >1995
 -Deviations from country_D



**National genetic trends are supposed to be better captured
with SD MACE**

ΔG biases: more visible with SD MACE than with S-MGS MACE

Consequence?

Some improvements are needed



ROBUST MACE (Ducrocq et al., 2003)

Country x Birth Year effect instead of Country effect



II. ROBUST MACE



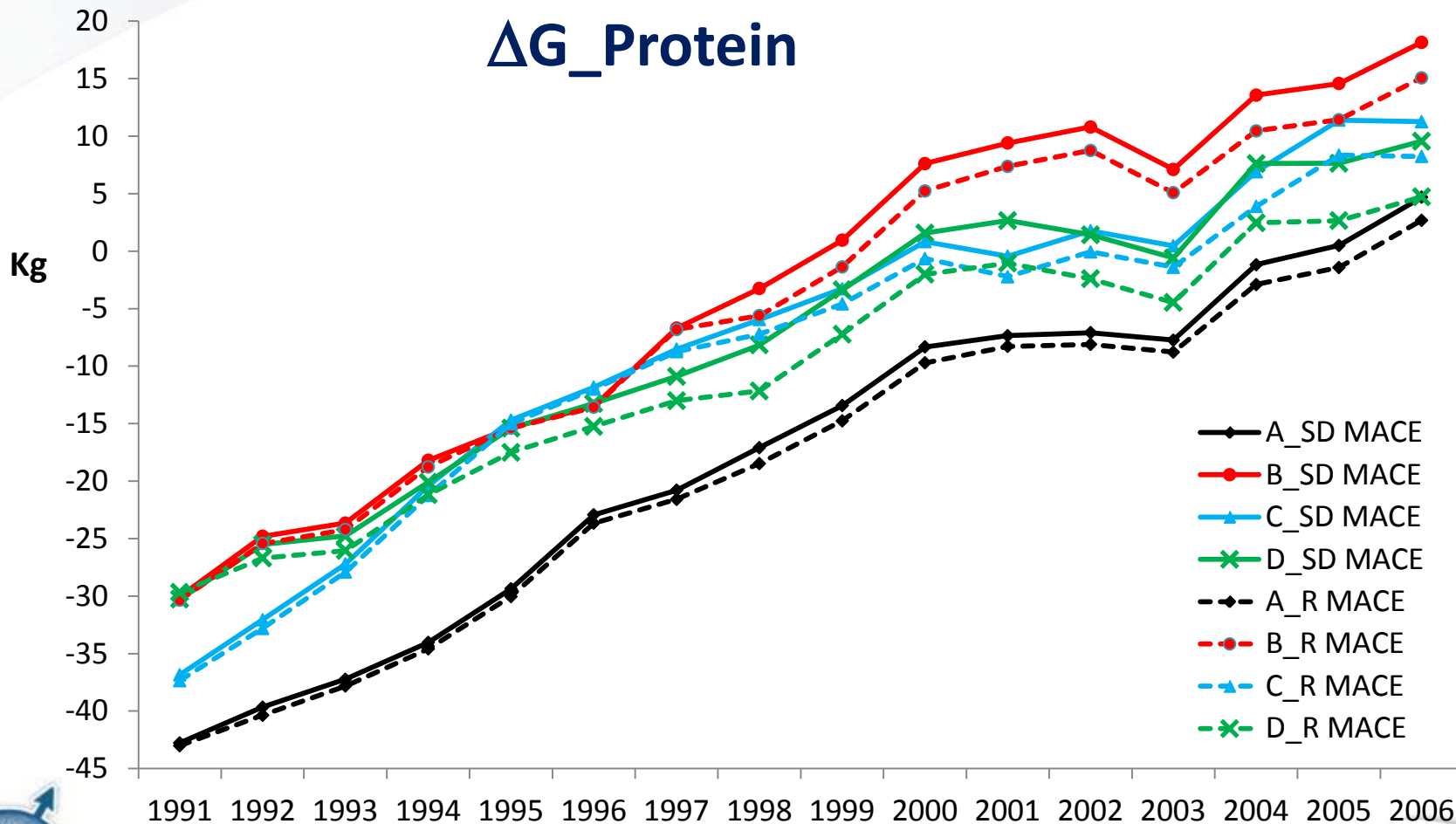


ROBUST MACE

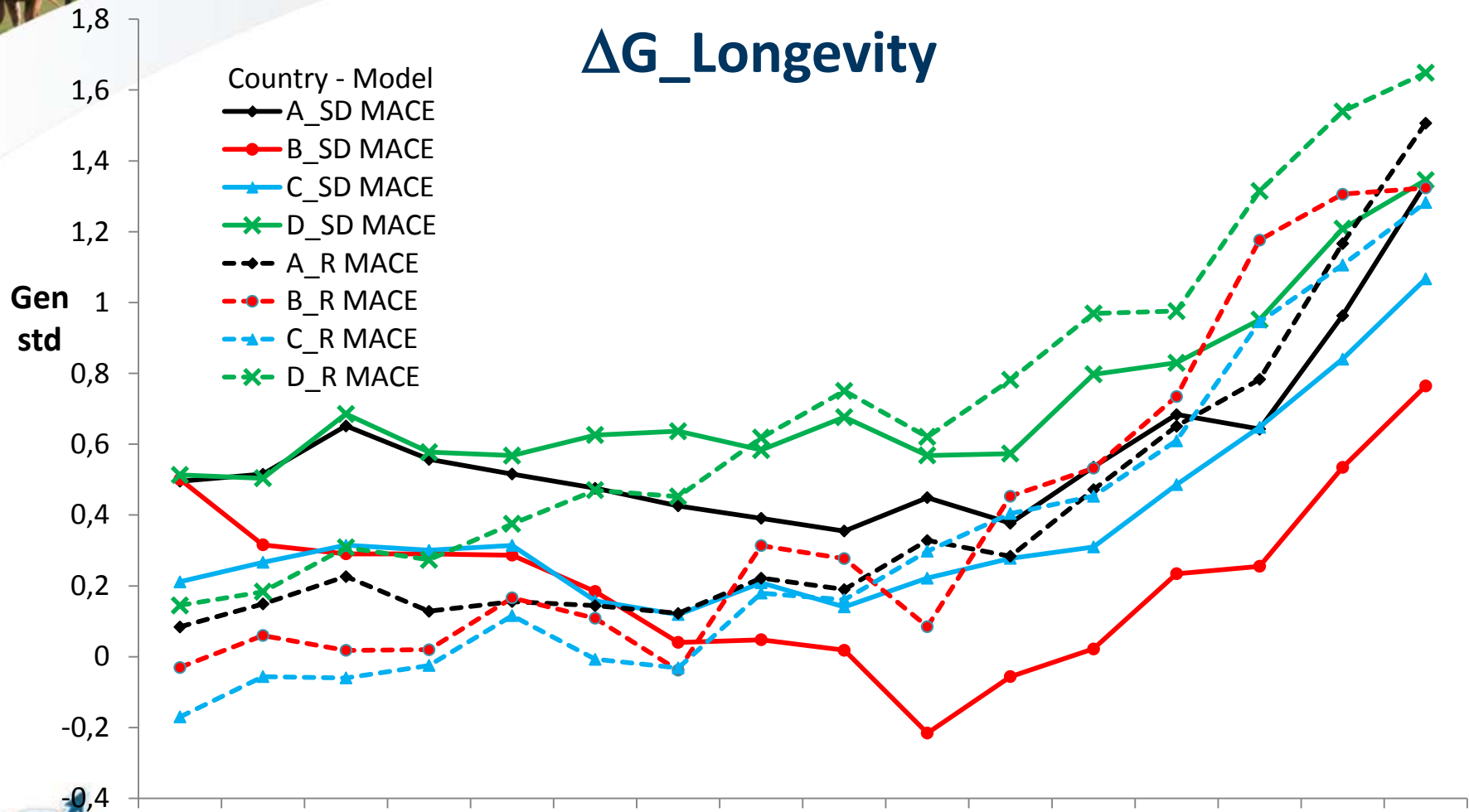
- ❑ Data from the April 2012 routine evaluation
- ❑ Country effect is replaced by Country x Birth Year effect
- ❑ Same within country sire variances and genetic correlations as in April 2012 routine evaluation.
- ❑ 7 country-period per country were created grouping bulls born within 3 consecutive years.

ROBUST MACE

$\Delta G_{\text{Protein}}$

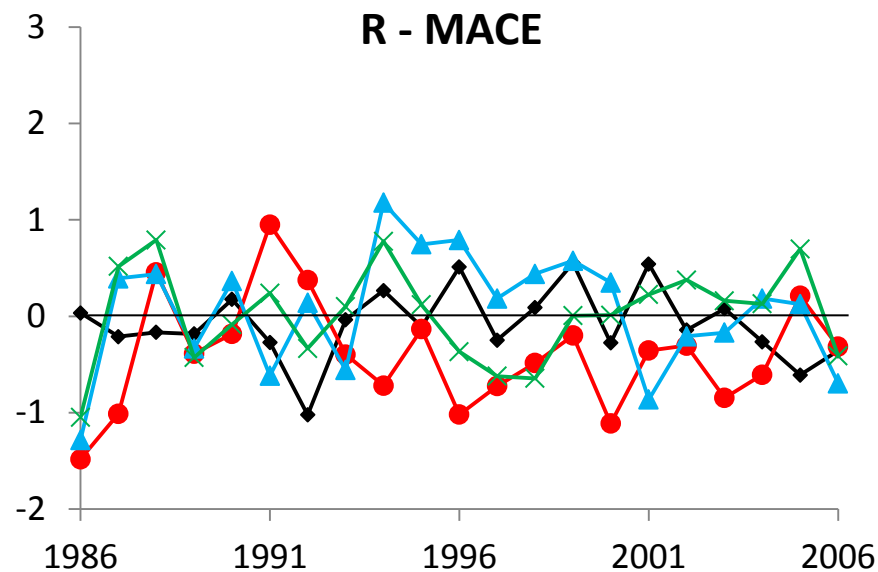
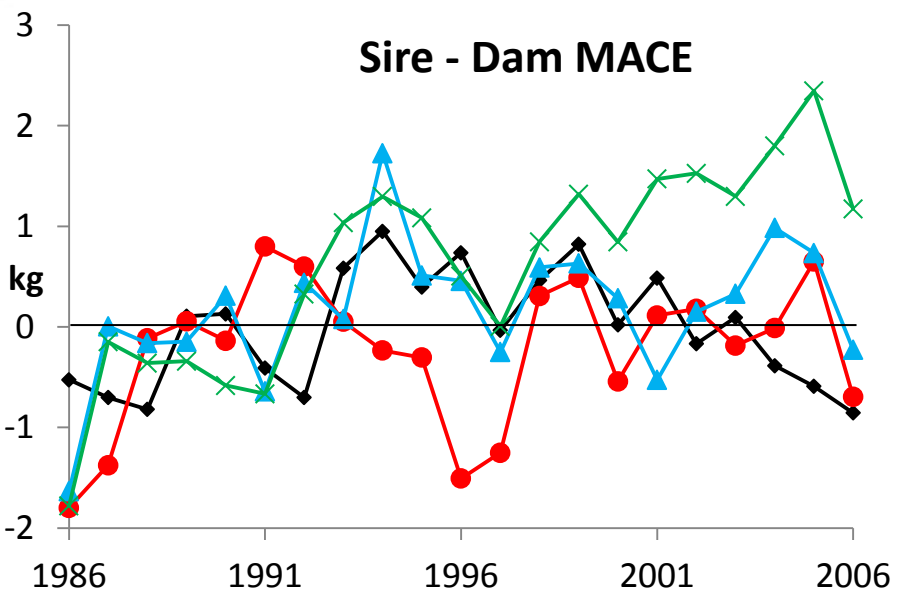


ROBUST MACE



Mendelian Samplings estimates

PROTEIN

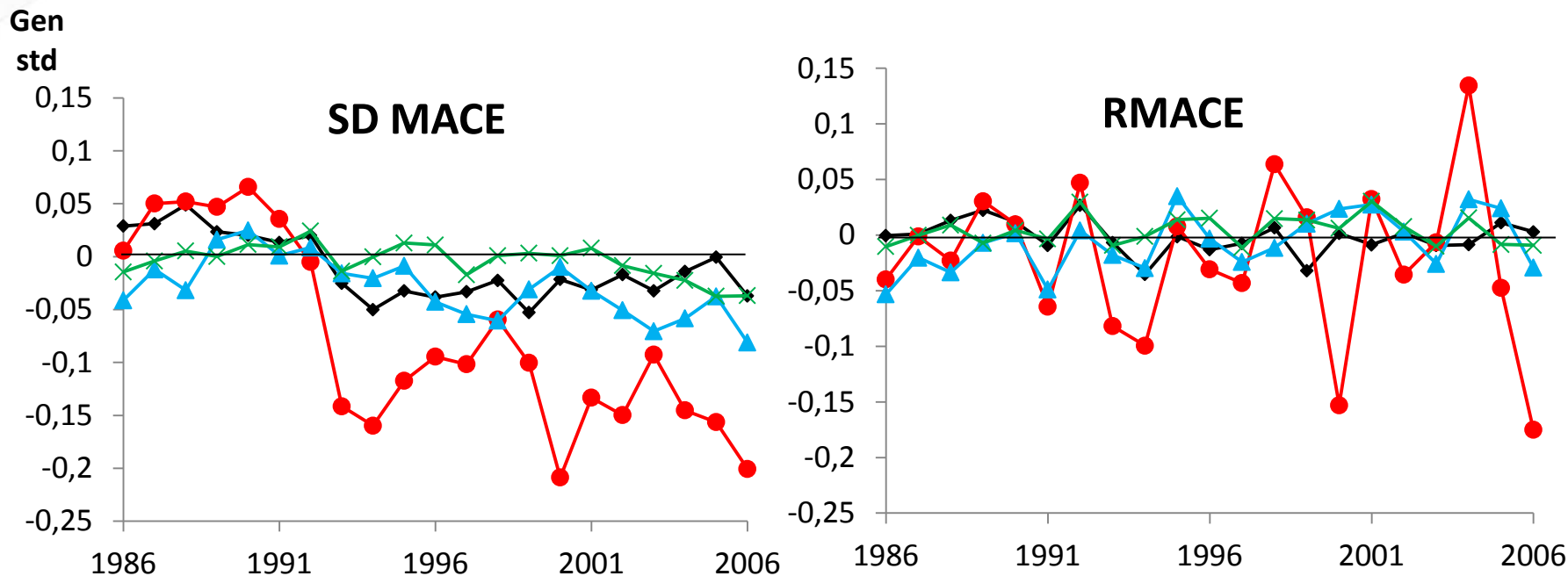


—◆— Country A —●— Country B
 —▲— Country C —×— Country D



Mendelian Samplings estimates

LONGEVITY



- Country A
- Country B
- ▲— Country C
- ×— Country D

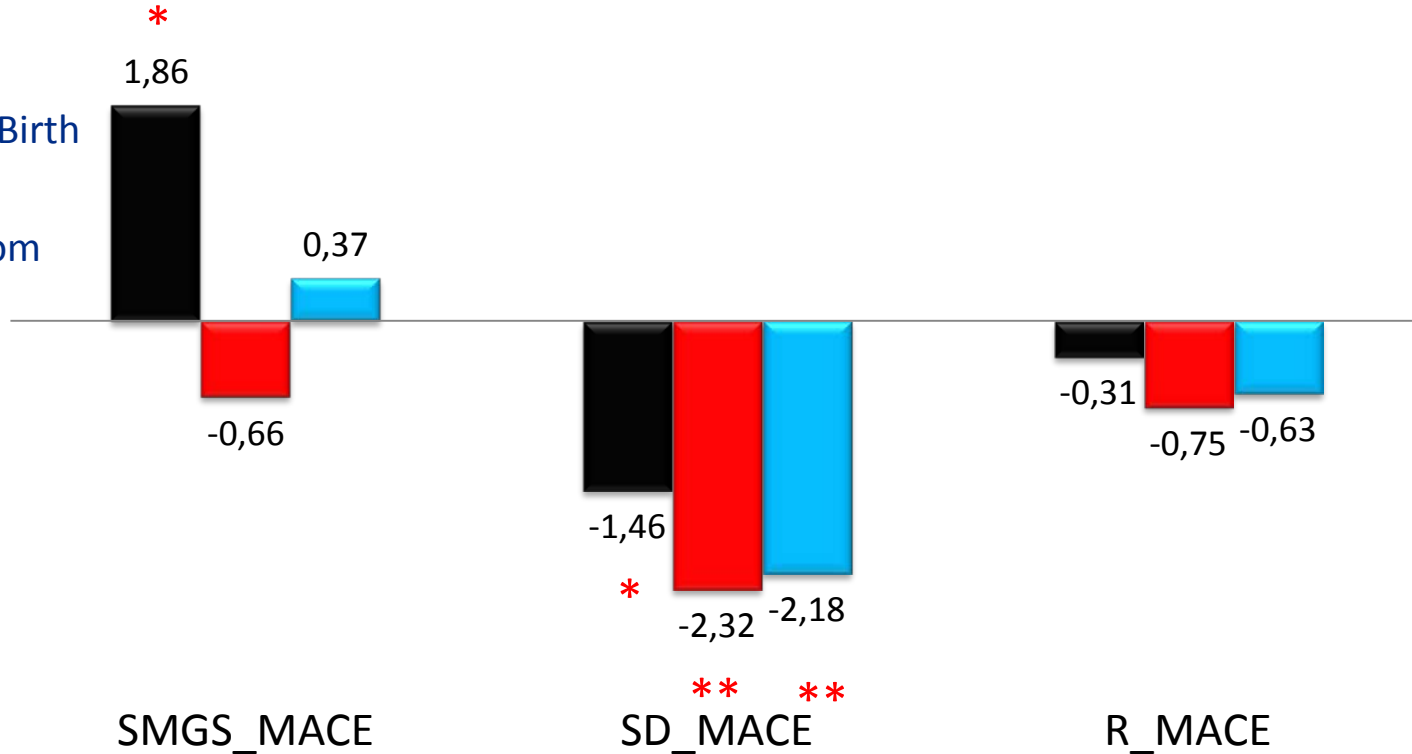


FULL SIBS

PROTEIN

■ Country_A ■ Country_B ■ country_C

-All bulls with Birth Year >1995
-Deviations from country_D

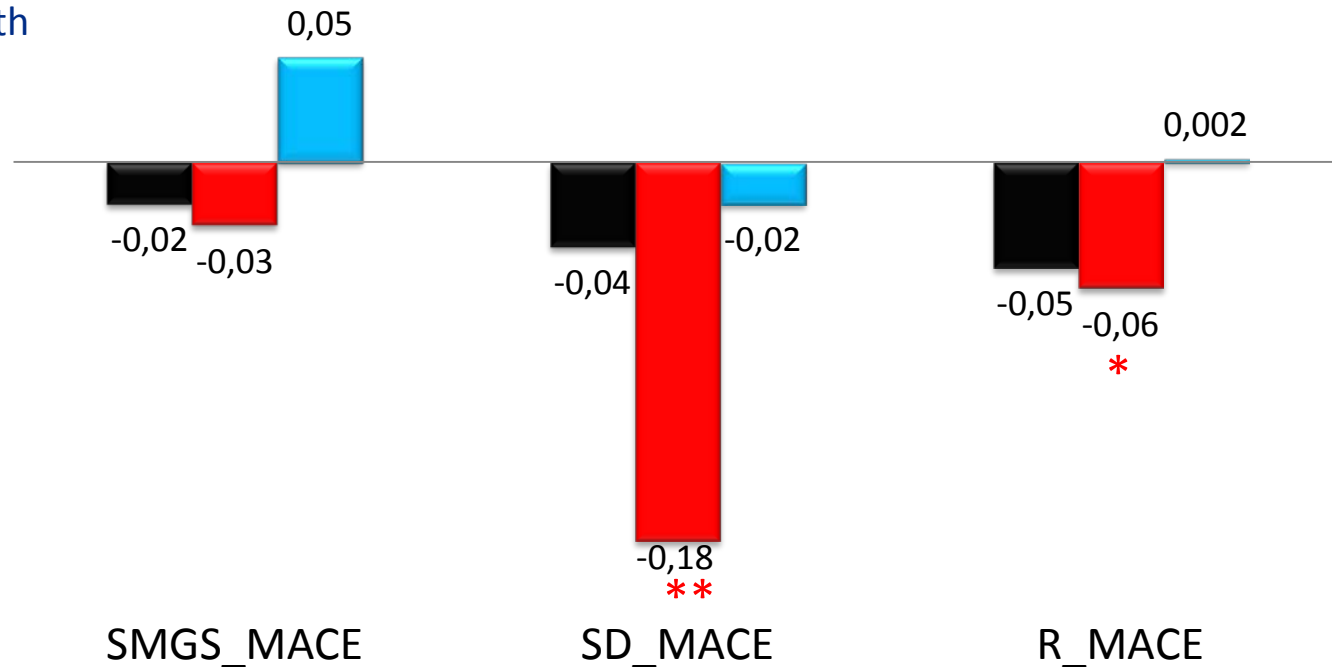


FULL SIBS

Longevity

■ Country_A ■ Country_B ■ country_C

-All bulls with Birth Year >1995
-Deviations from country_D





CONCLUSION

ROBUST MACE

- Ability to correct for the discrepancies on national genetic trends
- Easy to implement, does not need any new data



What is next?

- ❑ Separate country effects for each Birth Year
- ❑ Test the robustness of the model by simulating a systematic ΔG bias for one or several countries
- ❑ Study the impact of a country x year effect on estimated genetic correlations